

SEQUENCE LISTING

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<120> Methods for Inhibiting Angiogenesis in a Subject in Need Thereof

<130> MP.1.0239.PCT

<150> US 62/315,857

<151> 2016-03-31

<160> 71

<170> PatentIn version 3.5

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<221> CDS

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Leu Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro	
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Val Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn	
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gac cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg	197
Asp Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu	
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cgc ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag	245
Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu	
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
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Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
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Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
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Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
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Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
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Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
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<222> (22)..(2082)

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Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val	
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Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp	
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cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg cgc	195
Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg	
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Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr	
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gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg tgc	291
Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys	
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ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act ttc	339
Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe	
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Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser	
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Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp	
125 130 135	
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Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His	
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His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly	
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Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly	
175 180 185	

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Asp	Ala	Ser	Ala	Leu	Asp	Ile	Arg	Met	Gly	Thr	Leu	Lys	Arg	Leu	Ser	
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Tyr	Thr	His	Asp	Ala	Gly	Phe	Asp	Asn	Asp	Ile	Ala	Leu	Ile	Lys	Leu	
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Glu Lys Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys	
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gct ggc tta gaa agt ggg ggc aag gac agc tgc aga ggt gac agc gga	1923
Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly	
620 625 630	
ggg gca ctg gtg ttt cta gat agt gaa aca gag agg tgg ttt gtg gga	1971
Gly Ala Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly	
635 640 645 650	
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Gly Ile Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr	
655 660 665	
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Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile	
670 675 680	
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Ile Ser Asp Phe	
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Gly	Gly	Phe	Tyr	Cys	Ser	Cys	Arg	Ala	Gly	Tyr	Val	Leu	His	Arg	Asn
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Lys	Arg	Thr	Cys	Ser	Ala	Leu	Cys	Ser	Gly	Gln	Val	Phe	Thr	Gln	Arg
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Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
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Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
290 295 300

Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
305 310 315 320

Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
325 330 335

Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
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Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
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Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly

405

410

415

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
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Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
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Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
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Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
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Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
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Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
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Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly
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Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
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Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser
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Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr
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Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile
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Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro
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Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly
610 615 620

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
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Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
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50 55 60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
85 90 95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
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Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
145 150 155 160

Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
165 170 175

Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
210 215 220

Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
245 250 255

Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
275 280 285

Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
290 295 300

Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
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Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

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340 345 350

Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
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Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
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Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
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Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
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Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
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Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
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Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
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Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
485 490 495

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Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
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Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
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Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
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Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
565 570 575

Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
580 585 590

Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
595 600 605

Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
610 615 620

Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
625 630 635 640

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ccaccattc ttctacctac ccacccatc catccatcct tctatcagca tccttctacc	4860
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<210> 8
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 8

Met	Arg	Leu	Leu	Thr	Leu	Leu	Gly	Leu	Leu	Cys	Gly	Ser	Val	Ala	Thr
1			5					10						15	

Pro	Leu	Gly	Pro	Lys	Trp	Pro	Glu	Pro	Val	Phe	Gly	Arg	Leu	Ala	Ser
		20					25						30		

Pro	Gly	Phe	Pro	Gly	Glu	Tyr	Ala	Asn	Asp	Gln	Glu	Arg	Arg	Trp	Thr
		35					40					45			

Leu	Thr	Ala	Pro	Pro	Gly	Tyr	Arg	Leu	Arg	Leu	Tyr	Phe	Thr	His	Phe
	50					55					60				

Asp	Leu	Glu	Leu	Ser	His	Leu	Cys	Glu	Tyr	Asp	Phe	Val	Lys	Leu	Ser
65					70					75				80	

Ser	Gly	Ala	Lys	Val	Leu	Ala	Thr	Leu	Cys	Gly	Gln	Glu	Ser	Thr	Asp
			85						90					95	

Thr	Glu	Arg	Ala	Pro	Gly	Lys	Asp	Thr	Phe	Tyr	Ser	Leu	Gly	Ser	Ser
			100					105					110		

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala
130 135

<210> 9
<211> 181
<212> PRT
<213> Homo sapiens

<400> 9

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
1 5 10 15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val

130

135

140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
 145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
 165 170 175

Lys Arg Thr Cys Ser
 180

<210> 10
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
 1 5 10 15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
 20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
 35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
 50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
 65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
 85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
 100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
180 185 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
225 230 235 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
275 280 285

Trp Lys Ile His Tyr
290

<210> 11

<211> 41

<212> PRT
<213> Homo sapiens

<400> 11

Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys
1 5 10 15

Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg
20 25 30

Ala Gly Tyr Val Leu His Arg Asn Lys
35 40

<210> 12
<211> 242
<212> PRT
<213> Homo sapiens

<400> 12

Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val
1 5 10 15

Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn
20 25 30

Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala
35 40 45

Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His
50 55 60

Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr
65 70 75 80

His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn
85 90 95

Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys
100 105 110

Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly
115 120 125

Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val
130 135 140

Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys
145 150 155 160

Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly
165 170 175

Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala
180 185 190

Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile
195 200 205

Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val
210 215 220

Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser
225 230 235 240

Asp Phe

<210> 13
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13

Gly Lys Asp Ser Cys Arg Gly Asp Ala Gly Gly Ala Leu Val Phe Leu
1 5 10 15

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
1 5 10 15

<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp
1 5 10 15

Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser
20 25 30

Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln
35 40

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16

Thr Phe Arg Ser Asp Tyr Ser Asn
1 5

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17

Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
1 5 10 15

Ser Asn Glu Lys Pro Phe Thr Gly Phe
20 25

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18

Ile Asp Glu Cys Gln Val Ala Pro Gly
1 5

<210> 19
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 19

Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys
1 5 10 15

Arg Gly Asp Ser Gly Gly Ala Leu Val
20 25

<210> 20
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (51)..(797)

<400> 20
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 Met Ser
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ctg ttt cca tca ctc cct ctc ctt ctc ctg agt atg gtg gca gcg tct 104
 Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala Ala Ser
 5 10 15

tac tca gaa act gtg acc tgt gag gat gcc caa aag acc tgc cct gca 152
 Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys Pro Ala
 20 25 30

gtg att gcc tgt agc tct cca ggc atc aac ggc ttc cca ggc aaa gat 200
 Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly Lys Asp
 35 40 45 50

ggg cgt gat ggc acc aag gga gaa aag ggg gaa cca ggc caa ggg ctc 248
 Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln Gly Leu
 55 60 65

aga ggc tta cag ggc ccc cct gga aag ttg ggg cct cca gga aat cca 296
 Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly Asn Pro
 70 75 80

ggg cct tct ggg tca cca gga cca aag ggc caa aaa gga gac cct gga 344
 Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp Pro Gly
 85 90 95

aaa agt ccg gat ggt gat agt agc ctg gct gcc tca gaa aga aaa gct 392
 Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg Lys Ala
 100 105 110

ctg caa aca gaa atg gca cgt atc aaa aag tgg ctc acc ttc tct ctg 440
 Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe Ser Leu
 115 120 125 130

ggc aaa caa gtt ggg aac aag ttc ttc ctg acc aat ggt gaa ata atg 488

Gly	Lys	Gln	Val	Gly	Asn	Lys	Phe	Phe	Leu	Thr	Asn	Gly	Glu	Ile	Met	
				135					140					145		
acc	ttt	gaa	aaa	gtg	aag	gcc	ttg	tgt	gtc	aag	ttc	cag	gcc	tct	gtg	536
Thr	Phe	Glu	Lys	Val	Lys	Ala	Leu	Cys	Val	Lys	Phe	Gln	Ala	Ser	Val	
			150					155					160			
gcc	acc	ccc	agg	aat	gct	gca	gag	aat	gga	gcc	att	cag	aat	ctc	atc	584
Ala	Thr	Pro	Arg	Asn	Ala	Ala	Glu	Asn	Gly	Ala	Ile	Gln	Asn	Leu	Ile	
		165					170				175					
aag	gag	gaa	gcc	ttc	ctg	ggc	atc	act	gat	gag	aag	aca	gaa	ggg	cag	632
Lys	Glu	Glu	Ala	Phe	Leu	Gly	Ile	Thr	Asp	Glu	Lys	Thr	Glu	Gly	Gln	
	180					185					190					
ttt	gtg	gat	ctg	aca	gga	aat	aga	ctg	acc	tac	aca	aac	tgg	aac	gag	680
Phe	Val	Asp	Leu	Thr	Gly	Asn	Arg	Leu	Thr	Tyr	Thr	Asn	Trp	Asn	Glu	
195					200					205					210	
ggt	gaa	ccc	aac	aat	gct	ggt	tct	gat	gaa	gat	tgt	gta	ttg	cta	ctg	728
Gly	Glu	Pro	Asn	Asn	Ala	Gly	Ser	Asp	Glu	Asp	Cys	Val	Leu	Leu	Leu	
				215					220				225			
aaa	aat	ggc	cag	tgg	aat	gac	gtc	ccc	tgc	tcc	acc	tcc	cat	ctg	gcc	776
Lys	Asn	Gly	Gln	Trp	Asn	Asp	Val	Pro	Cys	Ser	Thr	Ser	His	Leu	Ala	
			230					235					240			
gtc	tgt	gag	ttc	cct	atc	tga	agggtcatat	cactcaggcc	ctccttgtct							827
Val	Cys	Glu	Phe	Pro	Ile											
				245												
ttttactgca	acccacaggc	ccacagtatg	cttgaaaaga	taaattatat	caatttcctc											887
atatccagta	ttgttccttt	tgtgggcaat	cactaaaaat	gatcactaac	agcaccaaca											947
aagcaataat	agt															960

<210> 21
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 21

Met	Ser	Leu	Phe	Pro	Ser	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Met	Val	Ala
1				5				10						15	

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys

20

25

30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
 35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
 50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
 65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
 85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
 100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
 115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
 130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
 145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
 165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
 180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
 195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
 210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X at position 1 represents hydroxyproline

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein X at position 4 represents hydrophobic residue

<400> 22

Xaa Gly Lys Xaa Gly Pro
1 5

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X represents hydroxyproline

<400> 23

Xaa Gly Lys Leu Gly
1 5

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (9)..(15)
<223> Wherein X at positions 9 and 15 represents hydroxyproline

<400> 24

Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa Gly
1 5 10 15

<210> 25
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(27)
<223> Wherein X at positions 3, 6, 15, 21, 24, 27 represents
hydroxyproline

<400> 25

Gly Pro Xaa Gly Pro Xaa Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly
1 5 10 15

Lys Leu Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa
20 25

<210> 26

<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (26)..(26)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (32)..(32)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (35)..(35)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (41)..(41)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (50)..(50)
<223> Xaa can be any naturally occurring amino acid

<400> 26

Gly Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly
1 5 10 15

Gln Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa
20 25 30

Gly Asn Xaa Gly Pro Ser Gly Ser Xaa Gly Pro Lys Gly Gln Lys Gly
35 40 45

Asp Xaa Gly Lys Ser
50

<210> 27
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(33)
<223> Wherein X at positions 3, 6, 12, 18, 21, 30, 33 represents
hydroxyproline

<400> 27

Gly	Ala	Xaa	Gly	Ser	Xaa	Gly	Glu	Lys	Gly	Ala	Xaa	Gly	Pro	Gln	Gly
1				5					10					15	

Pro	Xaa	Gly	Pro	Xaa	Gly	Lys	Met	Gly	Pro	Lys	Gly	Glu	Xaa	Gly	Asp
			20					25					30		

Xaa

<210> 28
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(45)
<223> Wherein X at positions 3, 6, 9, 27, 30, 36, 42, 45 represents
hydroxyproline

<400> 28

Gly	Cys	Xaa	Gly	Leu	Xaa	Gly	Ala	Xaa	Gly	Asp	Lys	Gly	Glu	Ala	Gly
1				5					10					15	

Thr Asn Gly Lys Arg Gly Glu Arg Gly Pro Xaa Gly Pro Xaa Gly Lys
20 25 30

Ala Gly Pro Xaa Gly Pro Asn Gly Ala Xaa Gly Glu Xaa
35 40 45

<210> 29
<211> 24
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<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29

Leu Gln Arg Ala Leu Glu Ile Leu Pro Asn Arg Val Thr Ile Lys Ala
1 5 10 15

Asn Arg Pro Phe Leu Val Phe Ile
20

<210> 30
<211> 559
<212> DNA
<213> Homo sapiens

<400> 30
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aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
ttcaccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240
tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc 300
cctggcaagg acactttcta ctcgtgggc tccagcctgg acattacctt ccgctccgac 360
tactccaacg agaagccgtt cacgggggtc gaggccttct atgcagccga ggacattgac 420
gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg 480
ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc 540

tcagccctgt gctccggcc 559

<210> 31
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<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31
cgggcacacc atgaggctgc tgaccctcct gggc 34

<210> 32
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<212> DNA
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<220>
<223> Synthetic

<400> 32
gacattacct tccgctccga ctccaacgag aag 33

<210> 33
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<220>
<223> Synthetic

<400> 33
agcagccctg aatacccacg gccgtatccc aaa 33

<210> 34
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<220>
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<400> 34
cgggatccat gaggctgctg accctc 26

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<220>
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<400> 35
ggaattccta ggctgcata 19

<210> 36
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<400> 36
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<210> 37
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<220>
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<400> 37
ggaattccta gtagtggat 19

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<400> 38
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<400> 40
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<400> 41
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<400> 42
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<400> 43
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<400> 44
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<210> 45
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<400> 45
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<400> 46
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<210> 47
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<223> Synthetic

<400> 47

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26

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48

Glu Pro Lys Ser Cys Asp Lys Thr His

1 5

<210> 49

<211> 4960

<212> DNA

<213> Homo Sapiens

<400> 49

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gctcgaaccc cggaggcaga ggtttggtgg ctcacacctg taatcccagc actttgagag 120

gctgaggcag gtgcatcgct ttggctcagg agttcaagac cagcctgggc aacacaggga 180

gacccccatc tctacaaaaa acaaaaacaa atataaaggg gataaaaaaa aaaaaaagac 240

aagacatgaa tccatgagga cagagtgtgg aagaggaagc agcagcctca aagttctgga 300

agctggaaga acagataaac aggtgtgaaa taactgcctg gaaagcaact tctttttttt 360

tttttttttt tttgagggtgg agtctcactc tgtcgtccag gctggagtgc agtggtgcga 420

tctcgatca ctgcaacctc cgcctcccag gctcaagcaa ttctcctgcc tcagcctccc 480

gagtagctgg gattataagt gcgcgctgcc acacctggat gattttttgta ttttagtag 540

agatgggatt tcacatggtt ggtcaggctg gtctcaaact cccaacctcg tgatccaccc 600

accttggcct cccaaagtgc tgggattaca ggtataagcc accgagccca gccaaaagcg 660

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<210> 50
 <211> 2090
 <212> DNA
 <213> Murine

<220>

<221> CDS

<222> (33)..(2090)

<400> 50

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				1				5			

ggc	ctg	ctg	tgg	agt	ttg	gtg	gcc	aca	ctt	ctg	ggc	tca	aag	tgg	cct	101
Gly	Leu	Leu	Trp	Ser	Leu	Val	Ala	Thr	Leu	Leu	Gly	Ser	Lys	Trp	Pro	
	10						15					20				

gaa	cct	gta	ttc	ggg	cgc	ctg	gtg	tcc	cct	ggc	ttc	cca	gag	aag	tat	149
Glu	Pro	Val	Phe	Gly	Arg	Leu	Val	Ser	Pro	Gly	Phe	Pro	Glu	Lys	Tyr	
	25					30					35					

gct	gac	cat	caa	gat	cga	tcc	tgg	aca	ctg	act	gca	ccc	cct	ggc	tac	197
Ala	Asp	His	Gln	Asp	Arg	Ser	Trp	Thr	Leu	Thr	Ala	Pro	Pro	Gly	Tyr	
40					45					50					55	

cgc	ctg	cgc	ctc	tac	ttc	acc	cac	ttt	gac	ctg	gaa	ctc	tct	tac	cgc	245
Arg	Leu	Arg	Leu	Tyr	Phe	Thr	His	Phe	Asp	Leu	Glu	Leu	Ser	Tyr	Arg	
			60						65					70		

tgc	gag	tat	gac	ttt	gtc	aag	ttg	agc	tca	ggg	acc	aag	gtg	ctg	gcc	293
Cys	Glu	Tyr	Asp	Phe	Val	Lys	Leu	Ser	Ser	Gly	Thr	Lys	Val	Leu	Ala	
			75					80					85			

aca	ctg	tgt	ggg	cag	gag	agt	aca	gac	act	gag	cag	gca	cct	ggc	aat	341
Thr	Leu	Cys	Gly	Gln	Glu	Ser	Thr	Asp	Thr	Glu	Gln	Ala	Pro	Gly	Asn	
		90					95					100				

gac	acc	ttc	tac	tca	ctg	ggc	ccc	agc	cta	aag	gtc	acc	ttc	cac	tcc	389
Asp	Thr	Phe	Tyr	Ser	Leu	Gly	Pro	Ser	Leu	Lys	Val	Thr	Phe	His	Ser	
	105					110					115					

gac	tac	tcc	aat	gag	aag	ccg	ttc	aca	ggg	ttt	gag	gcc	ttc	tat	gca	437
Asp	Tyr	Ser	Asn	Glu	Lys	Pro	Phe	Thr	Gly	Phe	Glu	Ala	Phe	Tyr	Ala	
120					125					130					135	

gcg	gag	gat	gtg	gat	gaa	tgc	aga	gtg	tct	ctg	gga	gac	tca	gtc	cct	485
Ala	Glu	Asp	Val	Asp	Glu	Cys	Arg	Val	Ser	Leu	Gly	Asp	Ser	Val	Pro	
			140						145					150		

tgt	gac	cat	tat	tgc	cac	aac	tac	ttg	ggc	ggc	tac	tat	tgc	tcc	tgc	533
Cys	Asp	His	Tyr	Cys	His	Asn	Tyr	Leu	Gly	Gly	Tyr	Tyr	Cys	Ser	Cys	
			155					160							165	

aga gcg ggc tac att ctc cac cag aac aag cac acg tgc tca gcc ctt	581
Arg Ala Gly Tyr Ile Leu His Gln Asn Lys His Thr Cys Ser Ala Leu	
170 175 180	
tgt tca ggc cag gtg ttc aca gga aga tct ggg tat ctc agt agc cct	629
Cys Ser Gly Gln Val Phe Thr Gly Arg Ser Gly Tyr Leu Ser Ser Pro	
185 190 195	
gag tac ccg cag cca tac ccc aag ctc tcc agc tgc acc tac agc atc	677
Glu Tyr Pro Gln Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile	
200 205 210 215	
cgc ctg gag gac ggc ttc agt gtc atc ctg gac ttc gtg gag tcc ttc	725
Arg Leu Glu Asp Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe	
220 225 230	
gat gtg gag acg cac cct gaa gcc cag tgc ccc tat gac tcc ctc aag	773
Asp Val Glu Thr His Pro Glu Ala Gln Cys Pro Tyr Asp Ser Leu Lys	
235 240 245	
att caa aca gac aag ggg gaa cac ggc cca ttt tgt ggg aag acg ctg	821
Ile Gln Thr Asp Lys Gly Glu His Gly Pro Phe Cys Gly Lys Thr Leu	
250 255 260	
cct ccc agg att gaa act gac agc cac aag gtg acc atc acc ttt gcc	869
Pro Pro Arg Ile Glu Thr Asp Ser His Lys Val Thr Ile Thr Phe Ala	
265 270 275	
act gac gag tcg ggg aac cac aca ggc tgg aag ata cac tac aca agc	917
Thr Asp Glu Ser Gly Asn His Thr Gly Trp Lys Ile His Tyr Thr Ser	
280 285 290 295	
aca gca cgg ccc tgc cct gat cca acg gcg cca cct aat ggc agc att	965
Thr Ala Arg Pro Cys Pro Asp Pro Thr Ala Pro Pro Asn Gly Ser Ile	
300 305 310	
tca cct gtg caa gcc acg tat gtc ctg aag gac agg ttt tct gtc ttc	1013
Ser Pro Val Gln Ala Thr Tyr Val Leu Lys Asp Arg Phe Ser Val Phe	
315 320 325	
tgc aag aca ggc ttc gag ctt ctg caa ggt tct gtc ccc ctg aaa tca	1061
Cys Lys Thr Gly Phe Glu Leu Leu Gln Gly Ser Val Pro Leu Lys Ser	
330 335 340	
ttc act gct gtc tgt cag aaa gat gga tct tgg gac cgg ccg atg cca	1109
Phe Thr Ala Val Cys Gln Lys Asp Gly Ser Trp Asp Arg Pro Met Pro	
345 350 355	
gag tgc agc att att gat tgt ggc cct ccc gat gac cta ccc aat ggc	1157
Glu Cys Ser Ile Ile Asp Cys Gly Pro Pro Asp Asp Leu Pro Asn Gly	

360	365	370	375	
cat gtg gac tat atc aca ggc cct caa gtg act acc tac aaa gct gtg				1205
His Val Asp Tyr Ile Thr Gly Pro Gln Val Thr Thr Tyr Lys Ala Val				
	380	385	390	
att cag tac agc tgt gaa gag act ttc tac aca atg agc agc aat ggt				1253
Ile Gln Tyr Ser Cys Glu Glu Thr Phe Tyr Thr Met Ser Ser Asn Gly		400	405	
	395			
aaa tat gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa				1301
Lys Tyr Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu		415	420	
	410			
aaa ctc ccc ccg gtt tgt gag cct gtt tgt ggg ctg tcc aca cac act				1349
Lys Leu Pro Pro Val Cys Glu Pro Val Cys Gly Leu Ser Thr His Thr		430	435	
	425			
ata gga gga cgc ata gtt gga ggg cag cct gca aag cct ggt gac ttt				1397
Ile Gly Gly Arg Ile Val Gly Gly Gln Pro Ala Lys Pro Gly Asp Phe		445	450	455
cct tgg caa gtc ttg ttg ctg ggt caa act aca gca gca gca ggt gca				1445
Pro Trp Gln Val Leu Leu Leu Gly Gln Thr Thr Ala Ala Ala Gly Ala		465	470	
	460			
ctt ata cat gac aat tgg gtc cta aca gcc gct cat gct gta tat gag				1493
Leu Ile His Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu		480	485	
	475			
aaa aga atg gca gcg tcc tcc ctg aac atc cga atg ggc atc ctc aaa				1541
Lys Arg Met Ala Ala Ser Ser Leu Asn Ile Arg Met Gly Ile Leu Lys		495	500	
	490			
agg ctc tca cct cat tac act caa gcc tgg ccc gag gaa atc ttt ata				1589
Arg Leu Ser Pro His Tyr Thr Gln Ala Trp Pro Glu Glu Ile Phe Ile		510	515	
	505			
cat gaa ggc tac act cac ggt gct ggt ttt gac aat gat ata gca ttg				1637
His Glu Gly Tyr Thr His Gly Ala Gly Phe Asp Asn Asp Ile Ala Leu		525	530	535
	520			
att aaa ctc aag aac aaa gtc aca atc aac gga agc atc atg cct gtt				1685
Ile Lys Leu Lys Asn Lys Val Thr Ile Asn Gly Ser Ile Met Pro Val		545	550	
	540			
tgc cta ccg cga aaa gaa gct gca tcc tta atg aga aca gac ttc act				1733
Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu Met Arg Thr Asp Phe Thr		560	565	
	555			

gga act gtg gct ggc tgg ggg tta acc cag aag ggg ctt ctt gct aga	1781
Gly Thr Val Ala Gly Trp Gly Leu Thr Gln Lys Gly Leu Leu Ala Arg	
570 575 580	

aac cta atg ttt gtg gac ata cca att gct gac cac caa aaa tgt acc	1829
Asn Leu Met Phe Val Asp Ile Pro Ile Ala Asp His Gln Lys Cys Thr	
585 590 595	

acc gtg tat gaa aag ctc tat cca gga gta aga gta agc gct aac atg	1877
Thr Val Tyr Glu Lys Leu Tyr Pro Gly Val Arg Val Ser Ala Asn Met	
600 605 610 615	

ctc tgt gct ggc tta gag act ggt ggc aag gac agc tgc aga ggt gac	1925
Leu Cys Ala Gly Leu Glu Thr Gly Gly Lys Asp Ser Cys Arg Gly Asp	
620 625 630	

agt ggg ggg gca tta gtg ttt cta gat aat gag aca cag cga tgg ttt	1973
Ser Gly Gly Ala Leu Val Phe Leu Asp Asn Glu Thr Gln Arg Trp Phe	
635 640 645	

gtg gga gga ata gtt tcc tgg ggt tcc att aat tgt ggg gcg gca ggc	2021
Val Gly Gly Ile Val Ser Trp Gly Ser Ile Asn Cys Gly Ala Ala Gly	
650 655 660	

cag tat ggg gtc tac aca aaa gtc atc aac tat att ccc tgg aat gag	2069
Gln Tyr Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Asn Glu	
665 670 675	

aac ata ata agt aat ttc taa	2090
Asn Ile Ile Ser Asn Phe	
680 685	

<210> 51
 <211> 685
 <212> PRT
 <213> Murine

<400> 51

Met Arg Leu Leu Ile Phe Leu Gly Leu Leu Trp Ser Leu Val Ala Thr
1 5 10 15

Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val Ser
20 25 30

Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
100 105 110

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Val
130 135 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145 150 155 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln Asn
165 170 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
180 185 190

Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val Ile
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala Gln
225 230 235 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser His
260 265 270

Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Gln
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro Val
420 425 430

Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Gln
450 455 460

Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu Thr
465 470 475 480

Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu Asn
485 490 495

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
500 505 510

Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
515 520 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
530 535 540

Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala Ser
545 550 555 560

Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu Thr
565 570 575

Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
580 585 590

Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro Gly
595 600 605

Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly Gly
610 615 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val Ile
660 665 670

Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
675 680 685

<210> 52
<211> 670
<212> PRT
<213> Murine

<400> 52

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1 5 10 15

Ser Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Ser Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Val Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln
145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
165 170 175

Arg Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val
195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala
210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser
245 250 255

His Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro
275 280 285

Thr Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp

325

330

335

Gly Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly
 340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
 355 360 365

Gln Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
 370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
 385 390 395 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro
 405 410 415

Val Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly
 420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
 435 440 445

Gln Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu
 450 455 460

Thr Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu
 465 470 475 480

Asn Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
 485 490 495

Ala Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala
 500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr
 515 520 525

Ile Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala
530 535 540

Ser Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu
545 550 555 560

Thr Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro
565 570 575

Ile Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro
580 585 590

Gly Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Ile Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
660 665 670

<210> 53
<211> 2091
<212> DNA
<213> Rat

<220>
<221> CDS
<222> (10)..(2067)

<400> 53
tggcacaca atg agg cta ctg atc gtc ctg ggt ctg ctt tgg agt ttg gtg
Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val

1	5	10	
gcc aca ctt ttg ggc tcc aag tgg cct gag cct gta ttc ggg cgc ctg			99
Ala Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu			
15	20	25	30
gtg tcc ctg gcc ttc cca gag aag tat ggc aac cat cag gat cga tcc			147
Val Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser			
	35	40	45
tgg acg ctg act gca ccc cct ggc ttc cgc ctg cgc ctc tac ttc acc			195
Trp Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr			
	50	55	60
cac ttc aac ctg gaa ctc tct tac cgc tgc gag tat gac ttt gtc aag			243
His Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys			
	65	70	75
ttg acc tca ggg acc aag gtg cta gcc acg ctg tgt ggg cag gag agt			291
Leu Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser			
	80	85	90
aca gat act gag cgg gca cct ggc aat gac acc ttc tac tca ctg ggt			339
Thr Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly			
95	100	105	110
ccc agc cta aag gtc acc ttc cac tcc gac tac tcc aat gag aag cca			387
Pro Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro			
	115	120	125
ttc aca gga ttt gag gcc ttc tat gca gcg gag gat gtg gat gaa tgc			435
Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys			
	130	135	140
aga aca tcc ctg gga gac tca gtc cct tgt gac cat tat tgc cac aac			483
Arg Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn			
	145	150	155
tac ctg ggc ggc tac tac tgc tcc tgc cga gtg ggc tac att ctg cac			531
Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His			
	160	165	170
cag aac aag cat acc tgc tca gcc ctt tgt tca ggc cag gtg ttc act			579
Gln Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr			
175	180	185	190
ggg agg tct ggc ttt ctc agt agc cct gag tac cca cag cca tac ccc			627
Gly Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro			
	195	200	205

aaa ctc tcc agc tgc gcc tac aac atc cgc ctg gag gaa ggc ttc agt	675
Lys Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser	
210 215 220	
atc acc ctg gac ttc gtg gag tcc ttt gat gtg gag atg cac cct gaa	723
Ile Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu	
225 230 235	
gcc cag tgc ccc tac gac tcc ctc aag att caa aca gac aag agg gaa	771
Ala Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu	
240 245 250	
tac ggc ccg ttt tgt ggg aag acg ctg ccc ccc agg att gaa act gac	819
Tyr Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp	
255 260 265 270	
agc aac aag gtg acc att acc ttt acc acc gac gag tca ggg aac cac	867
Ser Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His	
275 280 285	
aca ggc tgg aag ata cac tac aca agc aca gca cag ccc tgc cct gat	915
Thr Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp	
290 295 300	
cca acg gcg cca cct aat ggt cac att tca cct gtg caa gcc acg tat	963
Pro Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr	
305 310 315	
gtc ctg aag gac agc ttt tct gtc ttc tgc aag act ggc ttc gag ctt	1011
Val Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu	
320 325 330	
ctg caa ggt tct gtc ccc ctg aag tca ttc act gct gtc tgt cag aaa	1059
Leu Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys	
335 340 345 350	
gat gga tct tgg gac cgg ccg ata cca gag tgc agc att att gac tgt	1107
Asp Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys	
355 360 365	
ggc cct ccc gat gac cta ccc aat ggc cac gtg gac tat atc aca ggc	1155
Gly Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly	
370 375 380	
cct gaa gtg acc acc tac aaa gct gtg att cag tac agc tgt gaa gag	1203
Pro Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu	
385 390 395	
act ttc tac aca atg agc agc aat ggt aaa tat gtg tgt gag gct gat	1251
Thr Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp	

400	405	410	
gga ttc tgg acg agc tcc aaa gga gaa aaa tcc ctc ccg gtt tgc aag Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys 415 420 425 430			1299
cct gtc tgt gga ctg tcc aca cac act tca gga ggc cgt ata att gga Pro Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly 435 440 445			1347
gga cag cct gca aag cct ggt gac ttt cct tgg caa gtc ttg tta ctg Gly Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu 450 455 460			1395
ggt gaa act aca gca gca ggt gct ctt ata cat gac gac tgg gtc cta Gly Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu 465 470 475			1443
aca gcg gct cat gct gta tat ggg aaa aca gag gcg atg tcc tcc ctg Thr Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu 480 485 490			1491
gac atc cgc atg ggc atc ctc aaa agg ctc tcc ctc att tac act caa Asp Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln 495 500 505 510			1539
gcc tgg cca gag gct gtc ttt atc cat gaa ggc tac act cac gga gct Ala Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala 515 520 525			1587
ggt ttt gac aat gat ata gca ctg att aaa ctc aag aac aaa gtc aca Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr 530 535 540			1635
atc aac aga aac atc atg ccg att tgt cta cca aga aaa gaa gct gca Ile Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala 545 550 555			1683
tcc tta atg aaa aca gac ttc gtt gga act gtg gct ggc tgg ggg tta Ser Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu 560 565 570			1731
acc cag aag ggg ttt ctt gct aga aac cta atg ttt gtg gac ata cca Thr Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro 575 580 585 590			1779
att gtt gac cac caa aaa tgt gct act gcg tat aca aag cag ccc tac Ile Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr 595 600 605			1827

cca gga gca aaa gtg act gtt aac atg ctc tgt gct ggc cta gac cgc	1875
Pro Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg	
610 615 620	

ggt ggc aag gac agc tgc aga ggt gac agc gga ggg gca tta gtg ttt	1923
Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe	
625 630 635	

cta gac aat gaa aca cag aga tgg ttt gtg gga gga ata gtt tcc tgg	1971
Leu Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp	
640 645 650	

ggt tct att aac tgt ggg ggg tca gaa cag tat ggg gtc tac acg aaa	2019
Gly Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys	
655 660 665 670	

gtc acg aac tat att ccc tgg att gag aac ata ata aat aat ttc taa	2067
Val Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe	
675 680 685	

tttgcaaaaa aaaaaaaaaa aaaa	2091
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<210> 54
 <211> 685
 <212> PRT
 <213> Rat

<400> 54

Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val Ala Thr
1 5 10 15

Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val Ser
20 25 30

Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Thr
65 70 75 80

Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
100 105 110

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Thr
130 135 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145 150 155 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln Asn
165 170 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
180 185 190

Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile Thr
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala Gln
225 230 235 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser Asn
260 265 270

Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro Val
420 425 430

Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Glu
450 455 460

Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr Ala
465 470 475 480

Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp Ile
485 490 495

Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala Trp
500 505 510

Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly Phe
515 520 525

Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile Asn
530 535 540

Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu
545 550 555 560

Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr Gln
565 570 575

Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile Val
580 585 590

Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro Gly
595 600 605

Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly Gly
610 615 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val Thr
660 665 670

Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
675 680 685

<210> 55
<211> 670
<212> PRT
<213> Rat

<400> 55

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1 5 10 15

Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln
145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly

165

170

175

Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
 180 185 190

Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile
 195 200 205

Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala
 210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr
 225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser
 245 250 255

Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr
 260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro
 275 280 285

Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val
 290 295 300

Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
 305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
 325 330 335

Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly
 340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
 355 360 365

Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385 390 395 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro
405 410 415

Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly
420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
435 440 445

Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr
450 455 460

Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp
465 470 475 480

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala
485 490 495

Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
500 505 510

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
515 520 525

Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser
530 535 540

Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr
545 550 555 560

Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile

565

570

575

Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro
 580 585 590

Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly
 595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
 610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
 625 630 635 640

Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val
 645 650 655

Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
 660 665 670

<210> 56
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo Sapiens

<400> 56
 atgaggctgc tgaccctcct gggccttc

28

<210> 57
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo Sapiens

<400> 57
 gtgcccctcc tgcgtcacct ctg

23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 58
cagaggtgac gcaggagggg cac 23

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 59
ttaaaatcac taattatggt ctcgatc 27

<210> 60
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 60
atgaggctac tcattcttcct gg 22

<210> 61
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 61
ctgcagaggt gacgcagggg ggg 23

<210> 62

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 62
ccccccctgc gtcacctctg cag 23

<210> 63
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 63
ttagaaatta cttattatgt tctcaatcc 29

<210> 64
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat

<400> 64
gaggtgacgc aggaggggca ttagtgttt 29

<210> 65
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat

<400> 65
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<210> 66
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<220>

<223> Synthetic

<400> 66

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cagccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc      180
tacaggacat cgctgaagag caggctcacc atctccaagg acacctcaa aaaccagggtg      240
gtccttaca tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata      300
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<210> 67

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 67

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Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
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```

```
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
          20          25          30
```

```
Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
          35          40          45
```

```
Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
          50          55          60
```

```
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65          70          75          80
```

```
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
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85

90

95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
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Leu Val Thr Val Ser Ser
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<210> 68

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 68

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
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Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Thr
 20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
 100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser

115

120

<210> 69
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 69

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
 1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
 35 40 45

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 70
 <211> 324
 <212> DNA
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<220>
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<400> 70

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cagggcccctg tgttgggtcat ctatgatgat agcgaccggc cctcagggat ccctgaccga	180
ttctctgcct ccaactctgg gaacacggcc accctgacca tcactagggg cgaagccggg	240
gatgaggccg actattattg tcagggtgtgg gacattgcta ctgatcatgt ggtcttcggc	300
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<210> 71
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 71

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Thr	Ala	Thr	Ile	Thr	Cys	Ala	Gly	Asp	Asn	Leu	Gly	Lys	Lys	Arg	Val
			20					25						30	

His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			

Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Ala	Ser
	50					55					60				

Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Thr	Arg	Gly	Glu	Ala	Gly
65					70					75					80

Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ile	Ala	Thr	Asp	His
				85					90					95	

Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ala	Ala	Ala	Gly
			100					105						110	

Ser Glu Gln Lys Leu Ile Ser Glu
115 120